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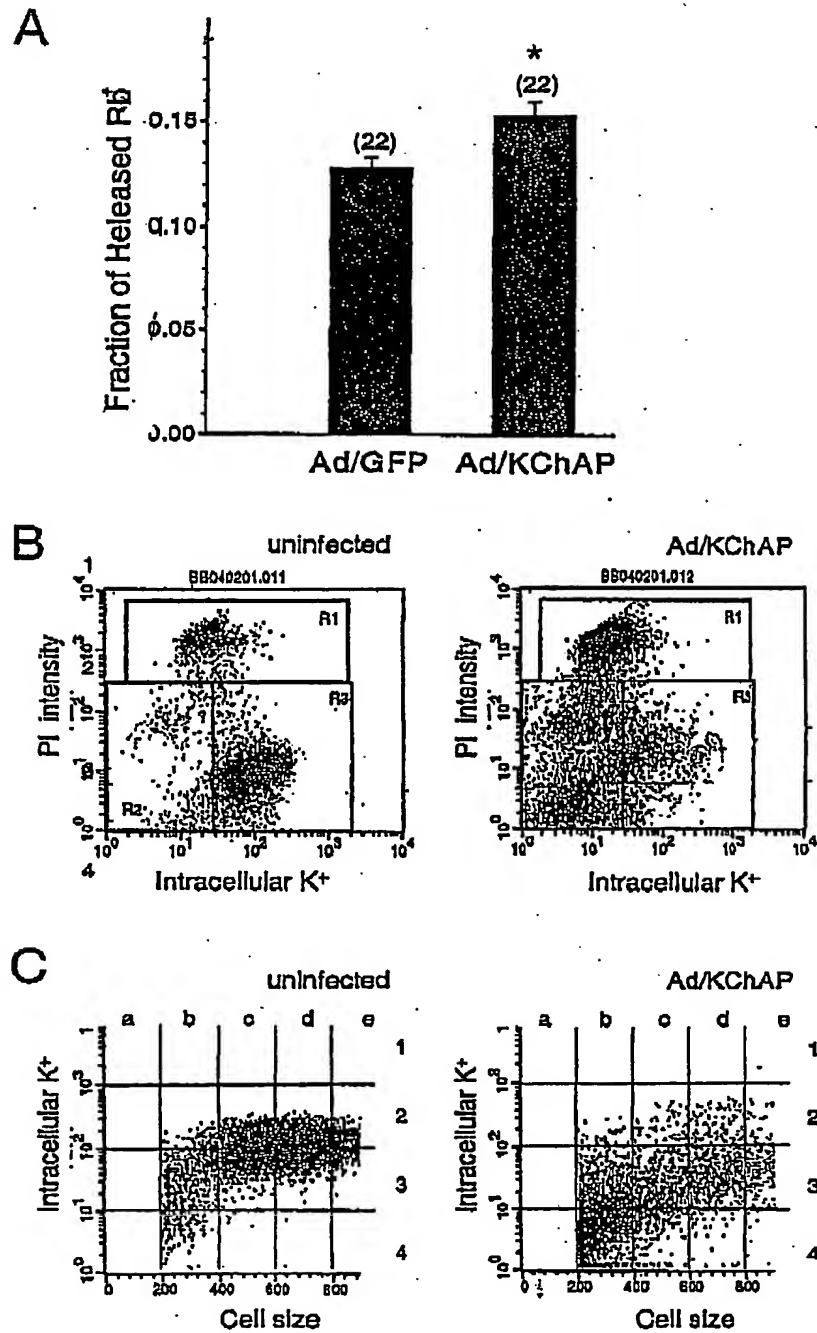


Fig. 1

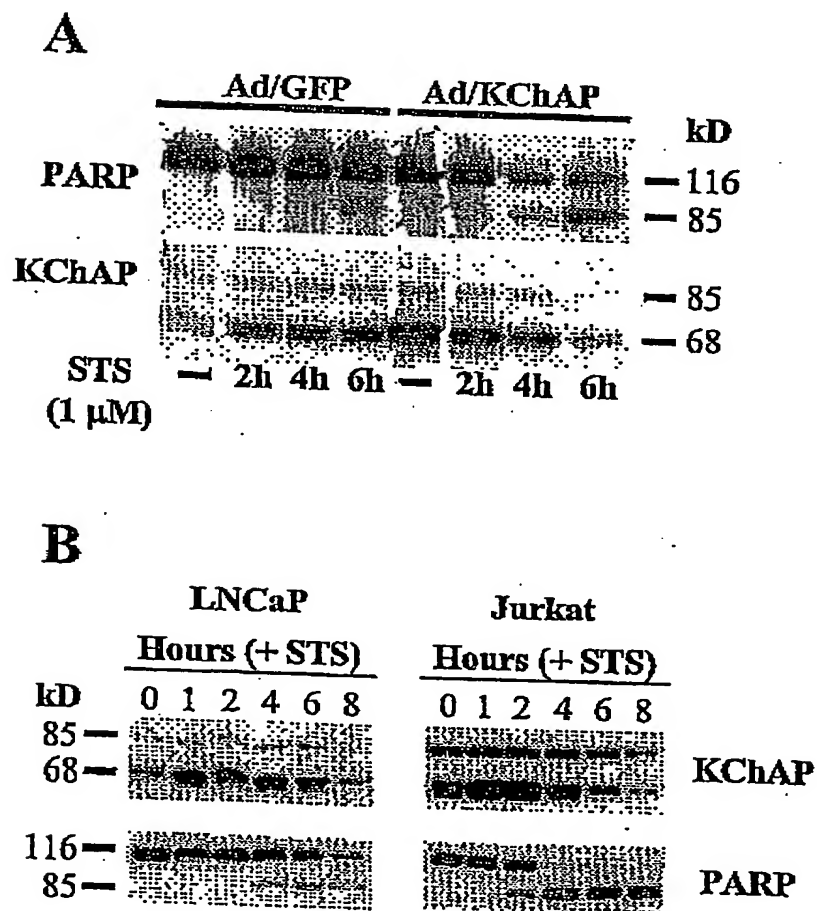


Fig. 2

Fig. 3

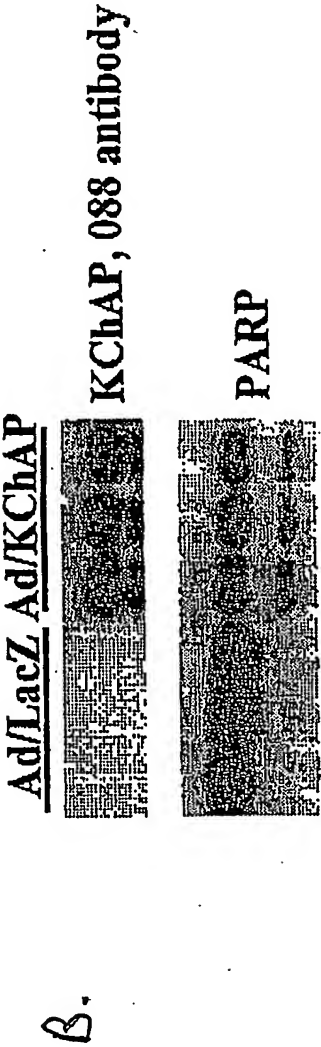
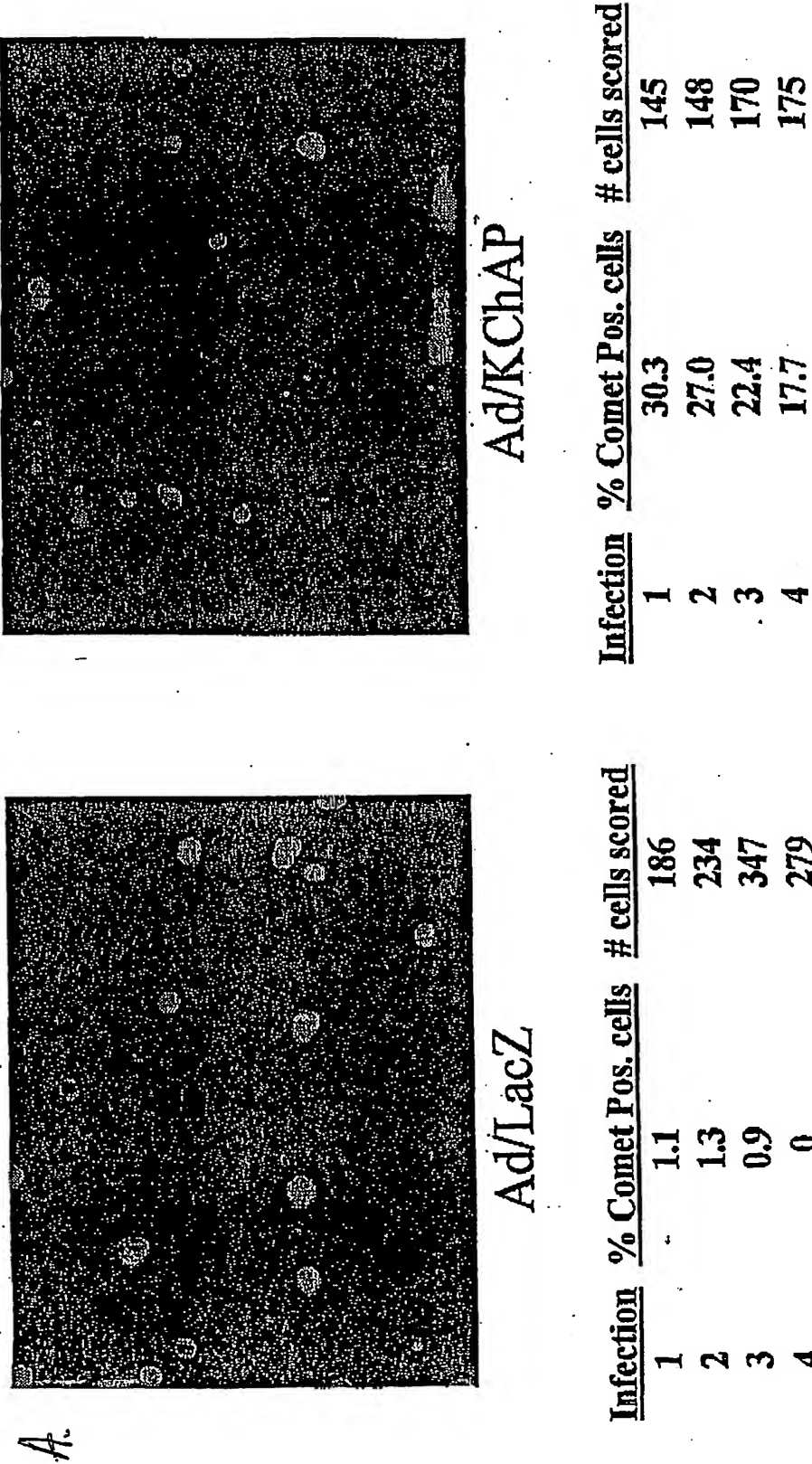


Fig. 4

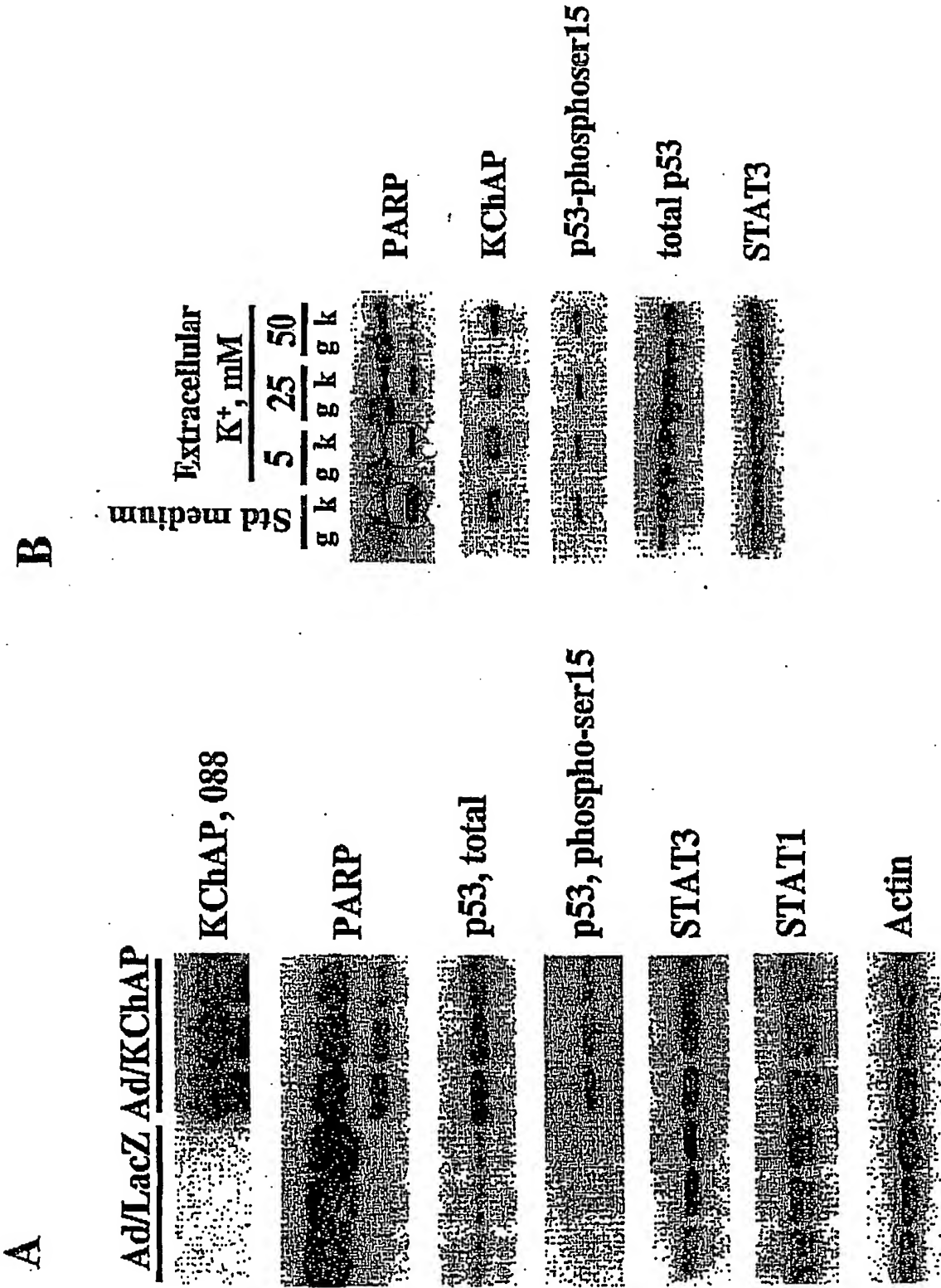


Fig. 5

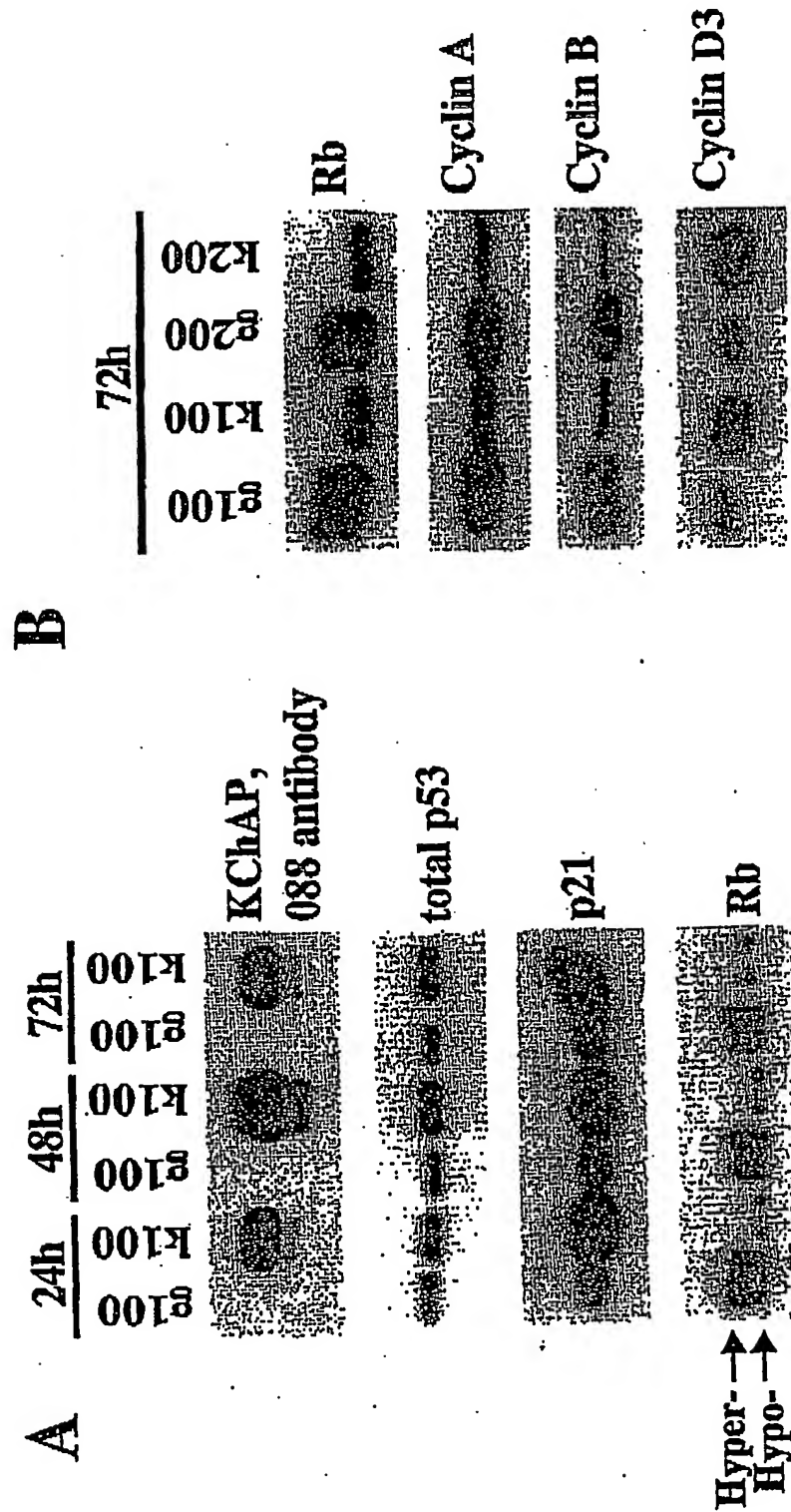
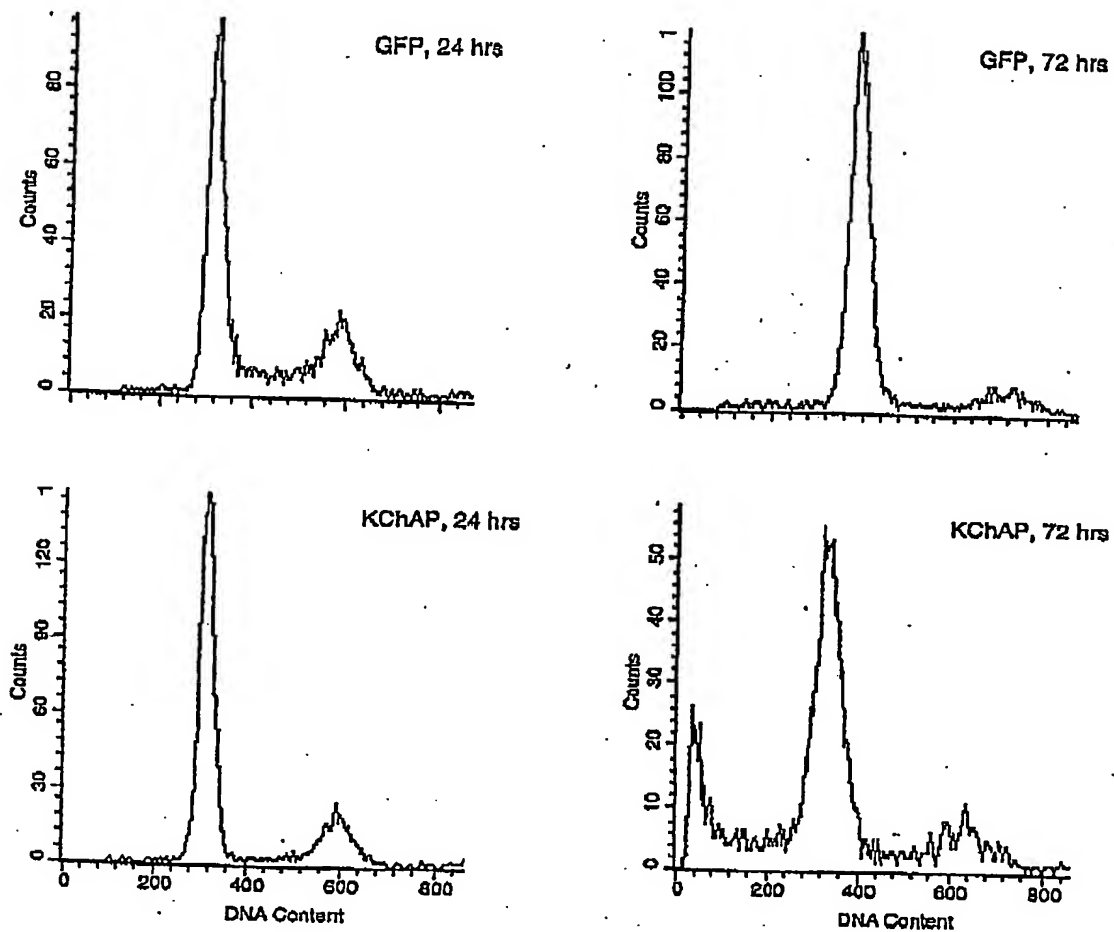


Fig. 6

A



B

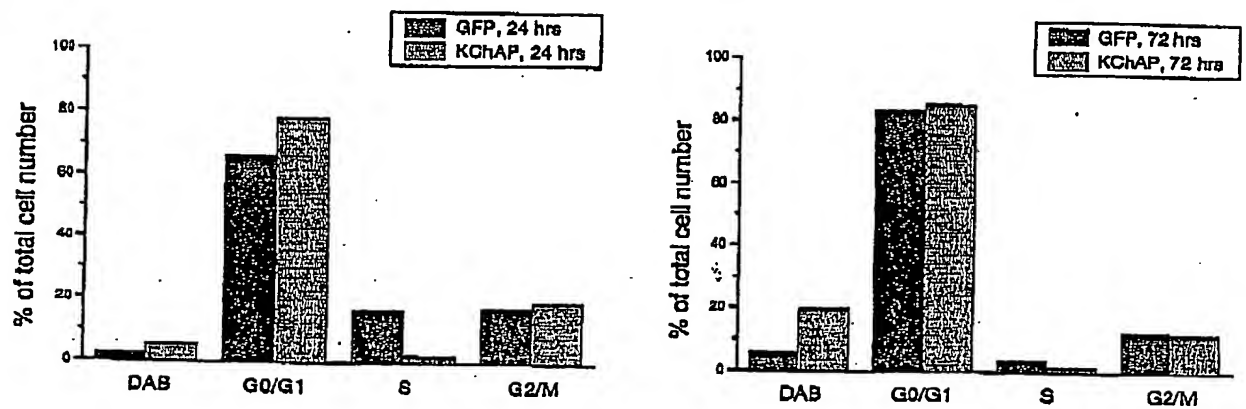


Fig. 7

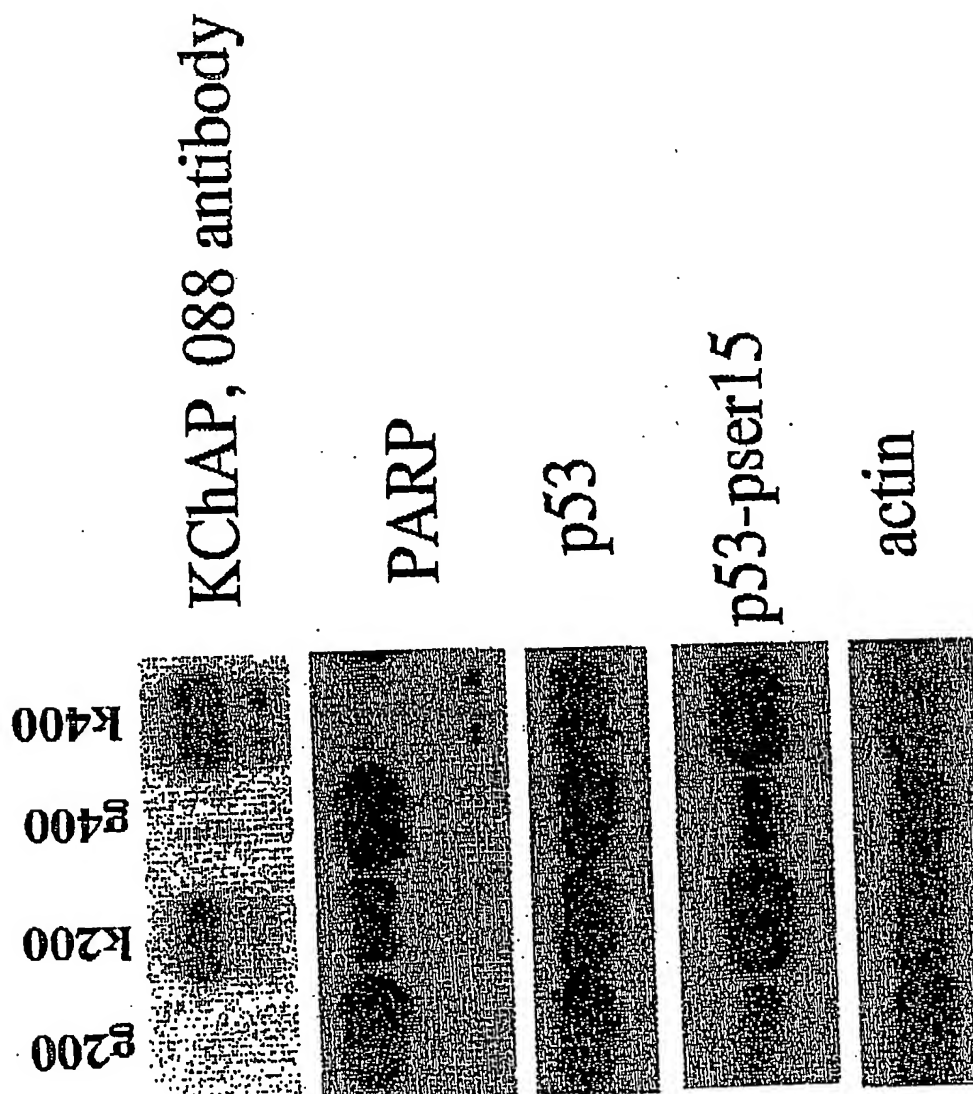


Fig. 8

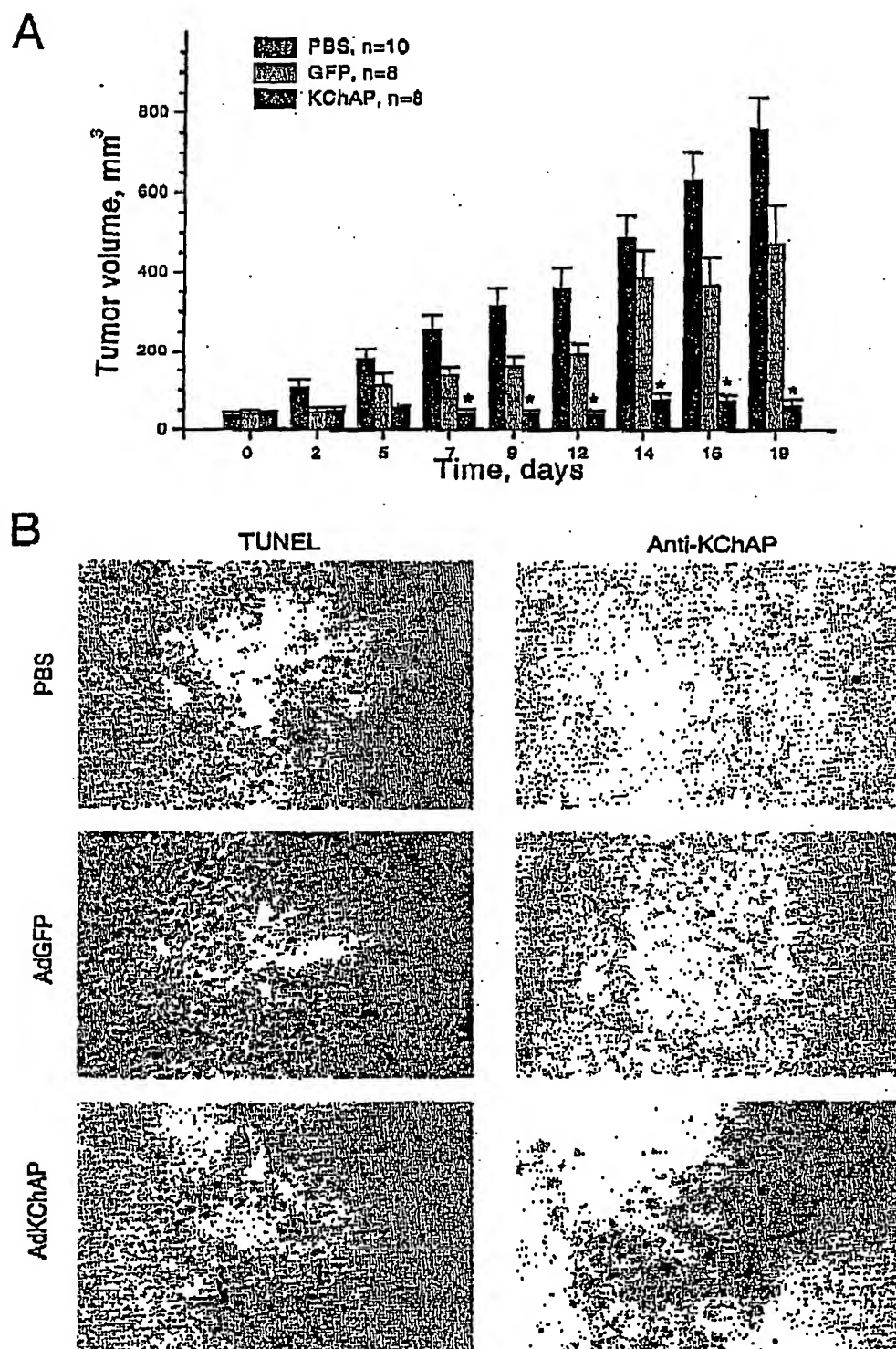


Fig. 9A

A
P
a
I

1 atgaagatcaaagagctttaccgacgacgctttccccggaagaccctggggccctctgat 60
-----+-----+-----+-----+-----+
M K I K E L Y R R R F P R K T L G P S D -

61 ctctcccttctctcttttggccctggcaccctctcctgtaggctcccttggtcctctagct 120
-----+-----+-----+-----+-----+
L S L L S L P P G T S P V G S P G P L A -

A
P
a
I

121 cccattcccccaacgctgttgccccctggcaccctgctgggcccccaagcgtgaggtggac 180
-----+-----+-----+-----+-----+
P I P P T L L A P G T L L G P K R E V D -

181 atgcacccccctctgccccagcctgtgcaccctgatgtcaccatgaaaccattgcccttc 240
-----+-----+-----+-----+-----+
M H P P L P Q P V H P D V T M K P L P F -

241 tatgaagtctatggggagctcatccggccaccacccttgcatccacttctagccagcgg 300
-----+-----+-----+-----+-----+
Y E V Y G E L I R P T T L A S T S S Q R -

301 tttgaggaagcgcactttacctttgccctcacacccagcaagtgcagcagattcttaca 360
-----+-----+-----+-----+-----+
F E E A H F T F A L T P Q Q V Q Q I L T -

361 tccagagaggttctgcccaggagccaaatgtgattataccatacaggtgcagctaaggttc 420
-----+-----+-----+-----+-----+
S R E V L P G A K C D Y T I Q V Q L R F -

P
V
u
I
I

421 tgtctctgtgagaccagctgccccaggaagattattttccccaacctctttgtcaag 480
-----+-----+-----+-----+-----+
C L C E T S C P Q E D Y F P P N L F V K -

Fig. 9B

B
s
t
E
I
I

gttaatgggaaactgtgccccctgccgggttaccttccccaaccaagaatggggccgag
481 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
V N G K L C P L P G Y L P P T K N G A E -

cccaagaggcccagccgcccccatcaacatcacacccctggctcgactctcagccactgtt
541 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
P K R P S R P I N I T P L A R L S A T V -

cccaacaccattgtggtcaattgggtcatctgagttcggacggaattactccttgtctgtg
601 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 660
P N T I V V N W S S E F G R N Y S L S V -

P
s
t
I

B
s
a
W
I

tacctggtgaggcagttgactgcaggaacccttctacaaaaactcagagcaaagggtatc
661 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 720
Y L V R Q L T A G T L L Q K L R A K G I -

cggaacccagaccactcgcgggcactgatcaaggagaaattgactgctgaccctgacagt
721 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 780
R N P D H S R A L I K E K L T A D P D S -

gaggtggccactacaagtctccgggtgtcactcatgtgcccgctaggggaagatgcgcctg
781 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 840
E V A T T S L R V S L M C P L G K M R L -

P
s
t
I

actgtcccttgtcggtgccctcacctgtgccacctgcagagcttcgatgctgccctttat
841 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 900
T V P C R A L T C A H L Q S F D A A L Y -

ctacagatgaatgagaagaagcctacatggacatgtcctgtgtgtgacaagaaggctccc
901 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 960
L Q M N E K K P T W T C P V C D K K A P -

tatgaatctcttatcattgatgggtttatattatggagattcttagttcctgttcagattgt
961 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1020
Y E S L I I D G L F M E I L S S C S D C -

Fig. 9C

P B
f a
l m
M H
I I

gatgagatccaattcatggaagatggatcctggtgcccaatgaaaccaagaaggaggca
1021-----+-----+-----+-----+-----+-----+ 1080
D E I Q F M E D G S W C P M K P K K E A -

P
f
l
M
I

tctgaggtttgcccccgccagggtatgggctggatggcctccagtacagcccaggtccag
1081-----+-----+-----+-----+-----+-----+ 1140
S E V C P P P G Y G L D G L Q Y S P V Q -

gggggagatccatcagagaataagaagaagggtcgaagttattgacttgacaatagaaagc
1141-----+-----+-----+-----+-----+-----+ 1200
G G D P S E N K K K V E V I D L T I E S -

P
v
u
I
I

tcatcagatgaggaggatctgccccctaccaagaagcactgttctgtcacctcagctgcc
1201-----+-----+-----+-----+-----+-----+ 1260
S S D E E D L P P T K K H C S V T S A A -

atcccgccctacctggaagcaaaggagtcctgacatctggccaccagccatcctcggtg
1261-----+-----+-----+-----+-----+-----+ 1320
I P A L P G S K G V L T S G H Q P S S V -

ctaaggagccctgctatgggcacgttgggtggggatttcctgtccagtcctccactacat

1321-----+-----+-----+-----+-----+-----+ 1380
L R S P A M G T L G G D F L S S L P L H -

gagtaccacctgccttcccactgggagccgacatccaaggtttagattttattttcattt
1381-----+-----+-----+-----+-----+-----+ 1400
E Y P P A F P L G A D I Q G L D L F S F -

cttcagacagagagtcagcactatggccccctctgtcatcacctcactagatgaacaggat
1441-----+-----+-----+-----+-----+-----+ 1500
L Q T E S Q H Y G P S V I T S L D E Q D -

Fig. 9D

A
p
a
I

```

gcccttggccacttcttccagtaccgagggacccttctcactttctgggcccactggcc
1501-----+-----+-----+-----+-----+-----+-----+ 1560
      A  L  G  H  F  F  Q  Y  R  G  T  P  S  H  F  L  G  P  L  A  -
                                     P          N
                                     s          a
                                     t          r
                                     I          I
cccacgctggggagctcccactgcagcgccactccggcgccccctcctggcgtgtcagc
1561-----+-----+-----+-----+-----+-----+-----+ 1620
      P  T  L  G  S  S  H  C  S  A  T  P  A  P  P  P  G  R  V  S  -
                                               S
                                               a
                                               u
                                               I
agcattgtggcccctgggggggccttgagggaggggcatggaggaccctgcctcaggt
1621-----+-----+-----+-----+-----+-----+-----+ 1680
      S  I  V  A  P  G  G  A  L  R  E  G  H  G  G  P  L  P  S  G  -

ccctctttgactggctgtcggtcagacatcatttccctggactga
1681-----+-----+-----+-----+-----+-----+ 1725
      P  S  L  T  G  C  R  S  D  I  I  S  L  D  *  -

```

Enzymes that do cut:

Apal	BamHI	BsaWI	BstEII	NarI	PflMI	PstI	PvuII
SauI							

Enzymes that do not cut:

AatII	AgeI	AseI	AvaI	BbrPI	BfrI	BglII	BsaBI
BsmI	BssHII	BstBI	BstXI	ClaI	DraI	DraIII	EagI
EcoRI	HindIII	HpaI	KpnI	MluI	NcoI	NdeI	NheI
NotI	NruI	NsiI	PmlI	PvuI	SacII	SalI	Scal
SfiI	SmaI	SnaBI	SpeI	SspI	StuI	XbaI	XhoI

Fig. 10

hPIAS1	MDGSELQKQYNEL	RVSEIQVLLGYAGRN	KHGRKHELLKALHL	LKAGCCFAVQMKIKE	LYERFPQIMTPAD	LSIPNVH-----S	82
mPIAS1F.....S.....A.....SS.A.S.....R.TIG.S.....L-----LSLPGT	82
mPIAS3F.....S.....D.MR.....S.....Y.RTLEBLS.....TIKSSVFSLOGG	75
hPIASx αFE.RN..S.F.....F.....S.....S.....Y.RTLEBLS.....TIKSSVFSLOGG	89
hPIASx βFE.RN..S.F.....F.....S.....S.....Y.RTLEBLS.....TIKSSVFSLOGG	89
hPIASy	MA.ELV.A.N...F.....D.M...FV..S.....V.R..Q.....VQFD...ELPK.....ET.YAK.NSE..P.....QPHRPL	81
hPIAS1	SPMPATLSPS---TI	EQUTYDGHPRASSPLL	PVSLGPRKLELPH	LTSALHFWHBDIKLQ	KLPTVDLLDELKPT	SLASDMSQRFTCTP	169
mPIAS1P.....E.....E.....E.....E.....E.....	169
mPIAS3VEPD.AVAGTHSL	STSVTP.SP...VG	S.L.QDT.PTF.MQ	FSFPFP.....VQ.K.N.....V.V.....T...TS...E.AH.	116
hPIASx αVEPD.AVAGTHSL	STSVTP.SP...VG	S.L.QDT.PTF.MQ	FSFPFP.....VQ.K.N.....V.V.....VQSSI...Q.KF.	179
hPIASx βVEPD.AVAGTHSL	STSVTP.SP...VG	S.L.QDT.PTF.MQ	FSFPFP.....VQ.K.N.....V.V.....VQSSI...Q.KF.	179
hPIASy	D.LTNHSTYDRAGAV	STPLA.FNIDY.V.	YGYK.NGLGR.....PATLTK.EVR.V.....FIM.....L.....E.VPQ.NEKLO.SPC	164
hPIAS1	AFALTRQVQOISSS	MD-1SGTKCDFTVQV	QLRFCLSETSCPOED	HFFPNLCVKNVTKPC	SLPGVLPFKNGVPEP	KRPSRPINITSLVRL	258
mPIAS1L...LT...REVLP.A...Y.I.....C.....Y.....F.....G.L.P.....A.....A.....RG.A--VRS..HPM.	258
mPIAS3L...LT...REVLP.A...Y.I.....C.....Y.....F.....G.L.P.....A.....A.....RG.A--VRS..HPM.	264
hPIASx αL...LT...REVLP.A...Y.I.....C.....Y.....F.....G.L.P.....A.....A.....RG.A--VRS..HPM.	269
hPIASx βL...LT...REVLP.A...Y.I.....C.....Y.....F.....G.L.P.....A.....A.....RG.A--VRS..HPM.	269
hPIASyR...EL.RKF.QGQF.V...A.....V.I.Y.D.....QY...IA.....HSY.V.....Y.SN.P.....C.....L.H.MZ.C.....L.H.MZ.	251
hPIAS1	STTVPTNMG-SWTAE	IGR---NYSRNVYL	VQLSSTVLLQSLRA	KGIENPHSRLIKE	KLTADPDSEIATTS	RVSLLCFLCHMRLTI	343
mPIAS1IVV.....S.....S.....S.....S.....S.....	344
mPIAS3	DS---QPLSFTFELL	HLSLGTTCPC.	R..TAGT...K.....V.....V.....PGVTHV.AR.....V	291
hPIASx αSA...QISI..AS..K---S.....	VR..T.AM.....EMM.....M.....M.....M.....	355
hPIASx βSA...QISI..AS..K---S.....	VR..T.AM.....EMM.....M.....M.....M.....	355
hPIASy	SAT-RITVT.GNY	-K---S..V.L..VR..T.SE.....	KT I.VK.ELCK.V..FL.....GV.....I..V...SVI..V...SVI..V...SV	335
hPIAS1	PCRALTCSTLQCFDA	TLYIQMNEKPTWQ	PDOKKAPVEHLID	GLFMEILKTDGDE	IQFKEDGTWAPWSK	KE-----VQEVIS	425
mPIAS1A.S.....T.....S.....S.....S.....S.....	426
mPIAS3A.S.....T.....S.....S.....S.....S.....	373
hPIASx αV.T.....I.....A.S.L.....ND.S.V.....K.Q..S.C.P.....NMK.....	437
hPIASx βV.T.....I.....A.S.L.....ND.S.V.....K.Q..S.C.P.....NMK.....	437
hPIASyE.A.....VF.....P.DQ.....LSK..SEZ.A.....EYLV..S.C.I.AE.....RSCSFQGAILVLG	425
hPIAS1	ASYN-GVDCGL----	SSTLEKQVA--SHHQ	SNKNKKVEVIDUTI	DSESS---DEEEEE--	-----PSAKETC	PSLSPTSP--LNKKG	491
mPIAS1N.....N.....N.....N.....N.....N.....	494
mPIAS3	PPPGY.L.....	QYSNV--QEGI	OPEEK.R.....L.PT.KQ.....SVT.AAL.AL.GS.....SVT.AAL.AL.GS.....	438
hPIASx α	SO-----PCTKIES	V.SKPCS--VTVA	EASK..D.....P.K.....IFM.E.QS--SPT.....IFM.E.QS--SPT.....	503
hPIASx β	SO-----PCTKIES	V.SKPCS--VTVA	EASK..D.....P.K.....IFM.E.QS--SPT.....IFM.E.QS--SPT.....	503
hPIASy	P.DAN.LLPAPSVNG	GA.GSTGGGPGVGS	ME.GKPGAD.V..LSSE.....EEEE	EEDEVEDEG.RP..R.	PFQKGLV.AC	510
hPIAS1	ILSLFHQASVSRTP	SLPAVDSYINTSLI	QDYRHEFH-MTP---	MPYDLQGLDFFPFLS	GDMJHVTSLAANA	AAVSDDDLLHSSRP	579
mPIAS1V.TSH..P.S.L.S.	AMTILGSDFLS---	---SL.V.EYP.AFP	LGA.I...L.S..Q	TES.Q.GP.VI---	---I.L.EQDTLGNP	580
mPIAS3	V.M--Y.P.S.-V..VTS..PAA.PP..T	---SV..H..ISS	SS..P.....SS..P.....SS..P.....SS..P.....	515
hPIASx α	V.M--Y.P.S.-V..VTS..PAA.PP..T	---SV..H..ISS	SS..P.....SS..P.....SS..P.....SS..P.....	550
hPIASx β	V.M--Y.P.S.-V..VTS..PAA.PP..T	---SV..H..ISS	SS..P.....SS..P.....SS..P.....SS..P.....	563
hPIAS1	FFVTSKMPFLQLEA	G-GTSLPTNGSSS	GSNSLSVS-SNSLSE	SHSHVTNRSTDTA	SIFGILPDISLD*	650	
mPIAS1A.....A.....G.G.AS.....A.....A.....	651	
mPIAS3	QYRGTPCR..GP.AP	TL..CHGSS.PAPPP	RV..I.AKSSS	G.GCPLSPGP	---LT.CES.V....	583	
hPIASx αEQRENDINH	E-LKLGTSSTVQ*	572	
hPIASx β	CPP.....S.TS	P-LTA.STSVTTT..	HES.TH...S.S.-	ETGV.I.SSG.N---	E.....	621	

Fig. 11

KChAP expression in Human Brain Tumors and Colon Cancers

C#64 C#65

HumI N T N T 46 54 61 64 71 85 86

